AMENDMENTS TO THE CLAIMS

Please cancel claims 1-75 without prejudice or disclaimer and please add new claims 76-92. The following listing of claims will replace all prior versions, and listings, of claims in the application:

Claims 1-75 (Cancelled)

76. (New) A peptide, which is a sequence variant and a functional and/or structural mimic of peptide YY, said peptide comprising at least one modification of the amino acid sequence set forth in SEQ ID NO: 2 (h-PYY 3-36), wherein said peptide

- includes a modification that conformationally constrains the relative position of the N-terminal amino acid of that part of SEQ ID NO 2 present in the peptide and amino acid 34 of SEQ ID NO: 2 in the peptide; and/or
- includes a branched amino acid sequence resulting in 2 free N-terminal amino acids; and/or
- includes N-terminal and/or C-terminal addition of a net basic amino acid sequence;
- optionally further includes deletion of amino acids 1-5 of SEQ ID NO: 2; and/or
- includes deletion of any one or more of amino acid residues 8-15 of SEQ ID NO: 2 without deletion of all of amino acids 1-7 of SEQ ID NO 2; and/or
- includes deletion of amino acids 6 and 7 of SEQ ID NO: 2 without deletion of all of amino acids 1-5 of SEQ ID NO 2; and/or
- includes deletion of amino acids 16-19 of SEQ ID NO: 2 without deletion of all of amino acids 1-15 of SEQ ID NO 2; and/or
- includes two cross linkable protected Cys amino acid substitutions; wherein said peptide further comprises at most 6 substitutions in the amino acid sequence set forth in SEQ ID NO: 2 , each of which is a structure and/or functionality preserving substitution.

77. (New) The peptide according to claim 76, wherein the modification that conformationally constrains the relative position of amino acids 1 and 34 of SEQ ID NO:

2 is selected from the group consisting of introduction of a disulfide bridge, introduction of a rigid bend involving positions corresponding to residues 9 and 10 in SEQ ID NO: 2, and introduction of at least one stabilizing amide bond between amino acid side chains.

78. (New) A peptide of formula I

R^1-X-Y-Z-A^{22}-A^{23}-A^{24}-A^{25}-A^{26}-A^{27}-A^{28}-A^{29}-A^{30}-A^{31}-A^{32}-A^{33}-A^{34}-A^{35}-A^{36}-R^2

(I)

wherein

A^{22} is Ala or a structure and/or functionality preserving substitution thereof;

A^{23} is Ser or a structure and/or functionality preserving substitution thereof;

A^{24} is Leu or a structure and/or functionality preserving substitution thereof, His or Cys;

A^{25} is Arg or a structure and/or functionality preserving substitution thereof;

A^{26} is Leu or a structure and/or functionality preserving substitution thereof, His or Cys;

A^{27} is Tyr or a structure and/or functionality preserving substitution thereof;

A^{28} is Leu or a structure and/or functionality preserving substitution thereof, or Cys;

A^{29} is Asn or a structure and/or functionality preserving substitution thereof; or Lys, which is optionally coupled to an amino acid sequence via a peptide bond at the c-amino group;

A^{30} is Leu or a structure and/or functionality preserving substitution thereof;

A^{31} is Val or a structure and/or functionality preserving substitution thereof, or Cys;

A^{32} is Thr or a structure and/or functionality preserving substitution thereof;

A^{33} is Arg or a structure and/or functionality preserving substitution thereof;

A^{34} is Gln or a structure and/or functionality preserving substitution thereof;

A^{35} is Arg or a structure and/or functionality preserving substitution thereof; and

A^{36} is Tyr or a structure and/or functionality preserving substitution thereof;

Z is a peptide of formula

A^{13}-A^{14}-A^{15}-A^{16}-A^{17}-A^{18}-A^{19}-A^{20}-A^{21}

which is absent or wherein,

A^{13} is Ser or a structure and/or functionality preserving substitution thereof or absent;

A^{14} is Pro or a structure and/or functionality preserving substitution thereof or absent;

A^{15} is Glu or a structure and/or functionality preserving substitution thereof or absent;

A^{16} is Glu or a structure and/or functionality preserving substitution thereof or absent;

A^{17} is Leu or a structure and/or functionality preserving substitution thereof or absent;

A^{18} is Asn or a structure and/or functionality preserving substitution thereof;

A^{19} is Arg or a structure and/or functionality preserving substitution thereof;

A^{20} is Tyr or a structure and/or functionality preserving substitution thereof; and

A^{21} is Tyr or a structure and/or functionality preserving substitution thereof;

Y is a peptide of formula

A^{8}-A^{9}-A^{10}-A-B

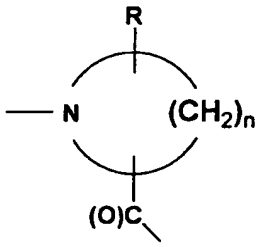
which is absent or wherein

A^{8} is Pro or a structure and/or functionality preserving substitution thereof;

A^{9} is Gly or a structure and/or functionality preserving substitution thereof;

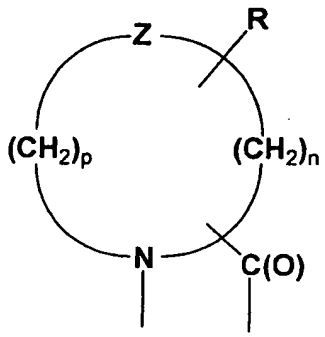
A^{10} is Glu or a structure and/or functionality preserving substitution thereof, or absent; and

A-B designates a dipeptide A^{11}-A^{12} selected from the group consisting of Gly-Gly, Pro-Gly, Gly-Pro, Sar-Sar, Sar-Hyp, Hyp-Sar, Pro-Sar, Sar-Pro, Pro-Hyp, Pro-Pro, Hyp-Pro, and Hyp-Hyp, where Pro and Hyp independently may be an L or D form, where the ring structure of Pro (III) and Hyp is optionally substituted with halogen, nitro, methyl, amino, or phenyl, Hyp represents 3-hydroxyproline or 4-hydroxyproline, Sar represents sarcosine, or one or both of the amino acid residues of A-B is a Sar, or an N-cyclohexylglycine residue, or A and B each independently represents a group of the formula II



(IIa)

wherein n is an integer having the value 3, 4, or 5, and R represents an optional substituent, preferably selected from the group consisting of halogen, phenyl, hydroxy, NH_2, and C(1-6)alkyl optionally substituted with halogen, or A-B designates the formula IIa



wherein n is an integer having the value 0, 1, 2, and 3, p is an integer having the value 0, 1, 2, and 3, Z represents 0 or S, and R represents an optional substituent, preferably selected from the group consisting of halogen, phenyl, hydroxy, NH_2, and C(1-6)alkyl, or A and B independently represents an amino acid residue having a saturated carbocyclic structure of 4, 5 or 6 members and where in said carbocyclic structure further comprises one or more heteroatoms,

X is a peptide of formula

A^3-A^4-A^5-A^6-A^7

which is absent or wherein

A^3 is Ile or a structure and/or functionality preserving substitution thereof, or Cys;

A^4 is Lys or a structure and/or functionality preserving substitution thereof;

A^5 is Pro or a structure and/or functionality preserving substitution thereof, or Cys;

A^6 is Glu or a structure and/or functionality preserving substitution thereof; and

A^7 is Ala or a structure and/or functionality preserving substitution thereof, or Cys;

R^1 is absent or an amino acid sequence; and

R^2 is absent or an amino acid sequence;

wherein said peptide comprises at most one disulfide bridge selected from Cys^3-S-S-Cys^{31}, Cys^3-S-S-Cys^{28}, Cys^5-S-S-Cys^{26}, and Cys^7-S-S-CYS^{24}

or wherein A is absent, Asp or a structure and/or functionality preserving substitution thereof and B is absent, Ala or a structure and/or functionality preserving substitution thereof and said peptide comprises a disulfide bridge selected from Cys^3-S-S-Cys^{31}, Cys^3-S-S-Cys^{28}, Cys^5-S-S-Cys^{26}, and Cys^7-S-S-Cys^{24};

wherein the number of structure and/or functionality preserving substitutions does not exceed 6;

wherein the C-terminal amino exposes a free carboxylic acid group or an amide group;

and

or a multimer and/or pharmaceutically acceptable salt thereof.

79. (New) The peptide according to claim 76, which binds with higher affinity to receptor Y2 than to receptor Y1.

80. (New) The peptide according to claim 76, which binds with higher affinity to receptor Y5 than to receptor Y 1.

81. (New) The peptide according to claim 78, wherein A^{29} is Lys.

82. (New) The peptide according to claim 81, wherein Lys^{29} is coupled to an amino acid sequence via a peptide bond at the E-amino group.

83. (New) The peptide according to claim 78, wherein at most one of A^{24}, A^{26}, A^{28}, and A^{31} is Cys.

84. (New) The peptide according to claim 78, comprising the disulfide bridge Cys^3-S-S-Cys^{31}, or comprising the disulfide bridge Cys^3-S-S-Cys^{28}, or comprising the disulfide bridge Cys^5-S-S-Cys^{26}, or comprising the disulfide bridge Cys^7-S-S-Cys^{24}.

85. (New) The peptide according to claim 78, wherein X has the amino acid sequence set forth in SEQ ID NO: 23 or wherein X is absent.

86. (New) The peptide according to claim 78, wherein A and B, independently are selected from the group consisting of N- and C(0)- radicals of the following compounds:

D/L-azetidin-3-carboxylic acid,

D/L-azetidin-2-carboxylic acid,

D/L-Indolin-2-carboxylic acid,

D/L-1,3-dihydro-isoindol-1-carboxylic acid,

D/L-thiazolidin-4-carboxylic acid,

D/L-pipecolinic acid,

D/L-nipecotinic acid,

isonipecotinic acid,

L/D-2-carboxymorpholin,

L/D-1,2,3,4-tetrahydroquinolin-3-carboxylic acid,

L/D-1,2,3,4-tetrahydroquinolin-3-carboxylic acid, and

4-carboxy-4-phenyl-piperidin.

87. (New) The peptide according to claim 78, wherein A-B designates 4-(2-aminoethyl)-6-dibenzofuranpropionic acid.

88. (New) The peptide according to claim 78, wherein A-B is a dipeptide or wherein A and B both designate Pro or a derivative thereof.

89. (New) The peptide according to claim 78, wherein A and B independently represents an amino acid residue having a saturated carbocyclic structure of 4, 5 or 6 members,

wherein said carbocyclic structure further comprises one or more heteroatoms selected from the group consisting of N, O and S.

90. (New) The peptide according to claim 78, wherein B, A^{13}, A^{14}, A^{15}, and A^{16} are absent, and optionally A^{10} A, and A^{17} are present, or wherein A^{10} A, B, A^{13}, A^{14}, A^{15}, A^{16}, and A^{17} are absent, and optionally A^{8}, A^{9}, A^{18}, A^{19}, A^{20}, and A^{21} are present.

91. (New) The peptide according to claim 78, wherein X is absent and Y and Z are present.

92. (New) A method for reducing or enhancing body weight in a subject, the method comprising administering, to the subject, an appropriately effective amount of (i) a peptide, which is a sequence variant and a functional and/or structural mimic of peptide YY, said peptide comprising at least one modification of the amino acid sequence set forth in SEQ ID NO: 2 (h-PYY 3-36), wherein said peptide

- includes a modification that conformationally constrains the relative position of the N-terminal amino acid of that part of SEQ ID NO 2 present in the peptide and amino acid 34 of SEQ ID NO: 2 in the peptide; and/or

- includes a branched amino acid sequence resulting in 2 free N-terminal amino acids; and/or

- includes N-terminal and/or C-terminal addition of a net basic amino acid sequence;

- optionally further includes deletion of amino acids 1-5 of SEQ ID NO: 2; and/or

- includes deletion of any one or more of amino acid residues 8-15 of SEQ ID NO: 2 without deletion of all of amino acids 1-7 of SEQ ID NO 2; and/or

- includes deletion of amino acids 6 and 7 of SEQ ID NO: 2 without deletion of all of amino acids 1-5 of SEQ ID NO 2; and/or

- includes deletion of amino acids 16-19 of SEQ ID NO: 2 without deletion of all of amino acids 1-15 of SEQ ID NO 2; and/or

- includes two cross linkable protected Cys amino acid substitutions; wherein said peptide further comprises at most 6 substitutions in the amino acid sequence set forth in

SEQ ID NO: 2 , each of which is a structure and/or functionality preserving substitution; or of (ii) a peptide of formula I

R^1-X-Y-Z-A^{22}-A^{23}-A^{24}-A^{25}-A^{26}-A^{27}-A^{28}-A^{29}-A^{30}-A^{31}-A^{32}-A^{33}-A^{34}-A^{35}-A^{36}-R^2

(I)

Wherein

A^{22} is Ala or a structure and/or functionality preserving substitution thereof;

A^{23} is Ser or a structure and/or functionality preserving substitution thereof;

A^{24} is Leu or a structure and/or functionality preserving substitution thereof, His or Cys;

A^{25} is Arg or a structure and/or functionality preserving substitution thereof;

A^{26} is Leu or a structure and/or functionality preserving substitution thereof, His or Cys;

A^{27} is Tyr or a structure and/or functionality preserving substitution thereof;

A^{28} is Leu or a structure and/or functionality preserving substitution thereof, or Cys;

A^{29} is Asn or a structure and/or functionality preserving substitution thereof, or Lys, which is optionally coupled to an amino acid sequence via a peptide bond at the s-amino group;

A^{30} is Leu or a structure and/or functionality preserving substitution thereof;

A^{31} is Val or a structure and/or functionality preserving substitution thereof, or Cys;

A^{32} is Thr or a structure and/or functionality preserving substitution thereof;

A^{33} is Arg or a structure and/or functionality preserving substitution thereof;

A^{34} is Gln or a structure and/or functionality preserving substitution thereof;

A^{35} is Arg or a structure and/or functionality preserving substitution thereof; and

A^{36} is Tyr or a structure and/or functionality preserving substitution thereof;

Z is a peptide of formula

A^{13}-A^{14}-A^{15}-A^{16}-A-^{17}-A^{18}-A^{19}-A^{20}-A^{21}

which is absent or wherein,

A^{13} is Ser or a structure and/or functionality preserving substitution thereof or absent;

A^{14} is Pro or a structure and/or functionality preserving substitution thereof or absent;

A^{15} is Glu or a structure and/or functionality preserving substitution thereof or absent;

A^{16} is Glu or a structure and/or functionality preserving substitution thereof or absent;

A^{17} is Leu or a structure and/or functionality preserving substitution thereof or absent;

A^{18} is Asn or a structure and/or functionality preserving substitution thereof;

A^{19} is Arg or a structure and/or functionality preserving substitution thereof;

A^{20} is Tyr or a structure and/or functionality preserving substitution thereof; and

A^{21} is Tyr or a structure and/or functionality preserving substitution thereof;

Y is a peptide of formula

A^{8}-A^{9}-A^{10}-A-B

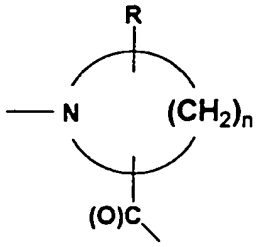
which is absent or wherein

A^{8} is Pro or a structure and/or functionality preserving substitution thereof;

A^{9} is Gly or a structure and/or functionality preserving substitution thereof,

A^{10} is Glu or a structure and/or functionality preserving substitution thereof, or absent; and

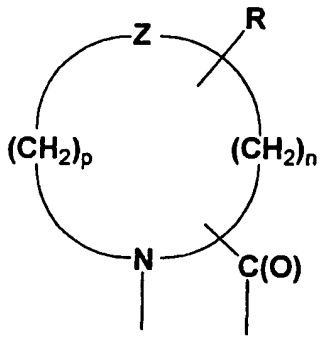
A-B designates a dipeptide A^{11}-A^{12} selected from the group consisting of Gly-Gly, Pro-Gly, Gly-Pro, Sar-Sar, Sar-Hyp, Hyp-Sar, Pro-Sar, Sar-Pro, Pro-Hyp, Pro-Pro, Hyp-Pro, and Hyp-Hyp, where Pro and Hyp independently may be an L or D form, where the ring structure of Pro and Hyp is optionally substituted with halogen, nitro, methyl, amino, or phenyl, Hyp represents 3-hydroxyproline or 4-hydroxyproline, Sar represents sarcosine, or one or both of the amino acid residues of A-B is a Sar, or an N-cyclohexylglycine residue, or A and B each independently represents a group of the formula II



(II)

wherein n is an integer having the value 3, 4, or 5, and R represents an optional substituent, preferably selected from the group consisting of halogen, phenyl, hydroxy, NH_2, and C(1-6)alkyl optionally substituted with halogen, or

A-B designates the formula IIa



wherein n is an integer having the value 0, 1, 2, and 3, p is an integer having the value 0, 1, 2, and 3, Z represents O or S, and R represents an optional substituent, preferably selected from the group consisting of halogen, phenyl, hydroxy, NH_2, and C(1-6)alkyl, or A and B independently represents an amino acid residue having a saturated carbocyclic structure of 4, 5 or 6 members and where in said carbocyclic structure further comprises one or more heteroatoms,

X is a peptide of formula

A^3-A^4-A^5-A^6-A^7

which is absent or wherein

A^3 is Ile or a structure and/or functionality preserving substitution thereof, or Cys;

A^4 is Lys or a structure and/or functionality preserving substitution thereof;

A^5 is Pro or a structure and/or functionality preserving substitution thereof, or Cys;

A^6 is Glu or a structure and/or functionality preserving substitution thereof; and

A^7 is Ala or a structure and/or functionality preserving substitution thereof, or Cys;

R^1 is absent or an amino acid sequence; and

R^2 is absent or an amino acid sequence;

wherein said peptide comprises at most one disulfide bridge selected from Cys^3-S-S-Cys^{31}, Cys^3-S-S-Cys^{28}, Cys^5-S-S-Cys^{26}, and Cys^7-S-S-Cys^{24};

or wherein A is absent, Asp or a structure and/or functionality preserving substitution thereof and B is absent, Ala or a structure and/or functionality preserving substitution thereof and said peptide comprises a disulfide bridge selected from Cys^3-S-S-Cys^{31}, Cys^3-S-S-Cys^{28}, Cys^5-S-S-Cys^{26}, and Cys^7-S-S-Cys^{24};

wherein the number of structure and/or functionality preserving substitutions does not exceed 6;

wherein the C-terminal amino exposes a free carboxylic acid group or an amide group; and

or a multimer and/or pharmaceutically acceptable salt thereof.